SEQUENCE LISTING

<110>   MCGILL UNIVERSITY
        GAGNON, Martin
        SARAGOVI, H. Uri

<120>   LIGANDS OF GANGLIOSIDE GD2 AND USES THEREOF

<130>   4810-70826-01

<140>   US 10/528,542
<141>   2003-09-19

<150>   US 60/412,492
<151>   2002-09-20

<160>   23

<170>   PatentIn version 3.2

<210>   1
<211>   13
<212>   PRT
<213>   Artificial

<220>
<223>   GD2 Ligand

<220>
<221>   MISC_FEATURE
<222>   (1)..(1)
<223>   Xaa = Absent or Tyr or an analogue thereof.

<220>
<221>   MOD_RES
<222>   (1)..(1)
<223>   The N-terminal group may be of the formula H2N-, RHN-, or, RRN-,
        wherein R at each occurence is independently selected from (C1-C6)
        alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6) alkyl,
        substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

<220>
<221>   MISC_FEATURE
<222>   (2)..(2)
<223>   Xaa = Absent or Cys or an analogue thereof.

<220>
<221>   MISC_FEATURE
<222>   (3)..(3)
<223>   Xaa = Gly or Tyr or an analogue thereof.

<220>
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<222>   (4)..(4)
<223>   Xaa = Gly or Cys or Tyr or an analogue thereof.

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<220>
<221>  MISC_FEATURE
<222>  (5)..(5)
<223>  Xaa = Ile or Cys or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (6)..(6)
<223>  Xaa = Thr or Ala or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (7)..(7)
<223>  Xaa = Asn or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (8)..(8)
<223>  Xaa = Tyr or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (9)..(9)
<223>  Xaa = Asn or Gly or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (10)..(10)
<223>  Xaa = Ser or Cys or Val or Thr or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (11)..(11)
<223>  Xaa = Ala or Cys or Tyr or His or Ser or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (12)..(12)
<223>  Xaa = absent or Leu or Cys or Tyr or an analogue thereof.


<220>
<221>  MISC_FEATURE
<222>  (13)..(13)
<223>  Xaa = absent or Met or Tyr or an analogue thereof.


<220>
<221>  MOD_RES
<222>  (13)..(13)
<223>  C-terminal grp is of the formula -C(O)OH, -C(O)R, -C(O)OR,
       -C(O)NHR, -C(O)NRR; wherein each R is independently selected from
       (C1-C6) alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6)
       alkyl, substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

<400>  1
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10
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<210>  2
<211>  13
<212>  PRT
<213>  Artificial

<220>
<223>  GD2 Ligand

<220>
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<222>  (1)..(1)
<223>  Xaa = Absent or Tyr or an analogue thereof.

<220>
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<222>  (2)..(2)
<223>  Xaa = Absent or Cys or an analogue thereof.

<220>
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<222>  (3)..(3)
<223>  Xaa = Gly or Tyr or an analogue thereof.

<220>
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<222>  (4)..(4)
<223>  Xaa = Gly or Cys or Tyr or an analogue thereof.

<220>
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<222>  (5)..(5)
<223>  Xaa = Ile or Cys or an analogue thereof.

<220>
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<222>  (6)..(6)
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<220>
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<223>  Xaa = Tyr or an analogue thereof.

<220>
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<223>  Xaa = Asn or Gly or an analogue thereof.

<220>
<221>  MISC_FEATURE
<222>  (10)..(10)
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<223> Xaa = Ser or Cys or Val or Thr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa = Ala or Cys or Tyr or His or Ser or an analogue thereof.

<220>
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<222> (12)..(12)
<223> Xaa = Absent or Leu or Cys or Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa = Absent or Met or Tyr or an analogue thereof.

<400> 2
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10

<210> 3
<211> 11
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 3
Gly Gly Ile Thr Asn Tyr Asn Ser Ala Leu Met
1   5   10

<210> 4
<211> 13
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 4
Tyr Cys Gly Gly Ile Thr Asn Tyr Asn Ser Ala Cys Tyr
1   5   10

<210> 5
<211> 10
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 5

Tyr Cys Ile Thr Asn Tyr Asn Ser Cys Tyr
1   5   10

<210> 6
<211> 11
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 6
Tyr Cys Gly Gly Ile Thr Asn Tyr Asn Cys Tyr
1   5   10

<210> 7
<211> 10
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 7
Tyr Cys Thr Asn Tyr Gly Val His Cys Tyr
1   5   10

<210> 8
<211> 9
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 8
Tyr Cys Thr Asn Tyr Gly Val Cys Tyr
1   5

<210> 9
<211> 9
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<400> 9
Gly Gly Ile Ala Asn Tyr Asn Thr Ser
1   5

<210> 10

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<211>   11
<212>   PRT
<213>   Artificial

<220>
<223>   GD2 Ligand

<400>   10
Tyr Cys Gly Gly Ile Ala Asn Tyr Asn Cys Tyr
1               5                   10


<210>   11
<211>   13
<212>   PRT
<213>   Artificial

<220>
<223>   GD2 Ligand

<400>   11
Tyr Cys Gly Gly Ile Ala Asn Tyr Asn Thr Ser Cys Tyr
1               5                   10


<210>   12
<211>   10
<212>   PRT
<213>   Artificial

<220>
<223>   GD2 Ligand

<400>   12
Tyr Cys Ile Ala Asn Tyr Asn Thr Cys Tyr
1               5                   10


<210>   13
<211>   5
<212>   PRT
<213>   Artificial

<220>
<223>   Spanning sequence for peptide analogs that actively inhibit
        GD2-mAb 3F8 interactions.

<400>   13
Ile Thr Asn Tyr Asn
1               5


<210>   14
<211>   5
<212>   PRT
<213>   Artificial
```

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<220>
<223>  Spanning sequence for peptide analogs that actively inhibit
       GD2-mAb 3F8 interactions.

<400>  14
Ile Ala Asn Tyr Asn
1               5


<210>  15
<211>  11
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(11)
<223>  Peptide is cyclic.

<400>  15
Cys Gly Gly Ile Thr Asn Tyr Asn Ser Ala Cys
1               5                   10


<210>  16
<211>  8
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(8)
<223>  Peptide is cyclic.

<400>  16
Cys Ile Thr Asn Tyr Asn Ser Cys
1               5


<210>  17
<211>  9
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(9)
<223>  Peptide is cyclic.
```

```
<400>  17
Cys Gly Gly Ile Thr Asn Tyr Asn Cys
1               5


<210>  18
<211>  8
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(8)
<223>  Peptide is cyclic.

<400>  18
Cys Thr Asn Tyr Gly Val His Cys
1               5


<210>  19
<211>  7
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(7)
<223>  Peptide is cyclic.

<400>  19
Cys Thr Asn Tyr Gly Val Cys
1               5


<210>  20
<211>  9
<212>  PRT
<213>  Artificial

<220>
<223>  Peptide Mimic

<220>
<221>  MISC_FEATURE
<222>  (1)..(9)
<223>  Peptide is cyclic.

<400>  20
Cys Gly Gly Ile Ala Asn Tyr Asn Cys
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<210> 21
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Peptide Mimic

<400> 21
Cys Gly Gly Ile Ala Asn Tyr Asn Thr Ser Cys
1   5   10

<210> 22
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Peptide mimic.

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> Peptide is cyclic.

<400> 22
Cys Ile Ala Asn Tyr Asn Thr Cys
1   5

<210> 23
<211> 1358
<212> PRT
<213> Homo sapiens

<400> 23
Met Gly Ala Asp Gly Glu Thr Val Val Leu Lys Asn Met Leu Ile Gly
1   5   10   15

Ile Asn Leu Ile Leu Leu Gly Ser Met Ile Lys Pro Ser Glu Cys Gln
            20   25   30

Leu Glu Val Thr Thr Glu Arg Val Gln Arg Gln Ser Val Glu Glu Glu
        35   40   45

Gly Gly Ile Ala Asn Tyr Asn Thr Ser Ser Lys Glu Gln Pro Val Val
    50   55   60

Phe Asn His Val Tyr Asn Ile Asn Val Pro Leu Asp Asn Leu Cys Ser
65   70   75   80

Ser Gly Leu Glu Ala Ser Ala Glu Gln Glu Val Ser Ala Glu Asp Glu
                85   90   95

9

```
Thr Leu Ala Glu Tyr Met Gly Gln Thr Ser Asp His Glu Ser Gln Val
        100                 105                 110

Thr Phe Thr His Arg Ile Asn Phe Pro Lys Lys Ala Cys Pro Cys Ala
        115                 120                 125

Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile Glu Met Leu
    130                 135                 140

Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala Asn Cys Cys
145                 150                 155                 160

Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro His Cys Ser
                165                 170                 175

Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile Cys Asn Glu
                180                 185                 190

Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro Leu Gly Cys
        195                 200                 205

Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys Asp Ser Glu
    210                 215                 220

Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr Asp Cys Ser
225                 230                 235                 240

Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu Glu Pro Tyr
                245                 250                 255

Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp Cys Ser Gly
                260                 265                 270

Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu Glu Gly Tyr Val
        275                 280                 285

Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala Cys Ser Gly Arg
    290                 295                 300

Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu Gly Tyr Gln Gly
305                 310                 315                 320

Pro Asp Cys Ser Ala Val Ala Pro Pro Glu Asp Leu Arg Val Ala Gly
                325                 330                 335

Ile Ser Asp Arg Ser Ile Glu Leu Glu Trp Asp Gly Pro Met Ala Val
                340                 345                 350

Thr Glu Tyr Val Ile Ser Tyr Gln Pro Thr Ala Leu Gly Gly Leu Gln
        355                 360                 365

Leu Gln Gln Arg Val Pro Gly Asp Trp Ser Gly Val Thr Ile Thr Glu
    370                 375                 380

Leu Glu Pro Gly Leu Thr Tyr Asn Ile Ser Val Tyr Ala Val Ile Ser
385                 390                 395                 400
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10

```
Asn Ile Leu Ser Leu Pro Ile Thr Ala Lys Val Ala Thr His Leu Ser
            405                 410                 415

Thr Pro Gln Gly Leu Gln Phe Lys Thr Ile Thr Glu Thr Thr Val Glu
            420                 425                 430

Val Gln Trp Glu Pro Phe Ser Phe Ser Phe Asp Gly Trp Glu Ile Ser
            435                 440                 445

Phe Ile Pro Lys Asn Asn Glu Gly Gly Val Ile Ala Gln Val Pro Ser
    450                 455                 460

Asp Val Thr Ser Phe Asn Gln Thr Gly Leu Lys Pro Gly Glu Glu Tyr
465                 470                 475                 480

Ile Val Asn Val Val Ala Leu Lys Glu Gln Ala Arg Ser Pro Pro Thr
            485                 490                 495

Ser Ala Ser Val Ser Thr Val Ile Asp Gly Pro Thr Gln Ile Leu Val
            500                 505                 510

Arg Asp Val Ser Asp Thr Val Ala Phe Val Glu Trp Ile Pro Pro Arg
            515                 520                 525

Ala Lys Val Asp Phe Ile Leu Leu Lys Tyr Gly Leu Val Gly Gly Glu
    530                 535                 540

Gly Gly Arg Thr Thr Phe Arg Leu Gln Pro Pro Leu Ser Gln Tyr Ser
545                 550                 555                 560

Val Gln Ala Leu Arg Pro Gly Ser Arg Tyr Glu Val Ser Val Ser Ala
            565                 570                 575

Val Arg Gly Thr Asn Glu Ser Asp Ser Ala Thr Thr Gln Phe Thr Thr
            580                 585                 590

Glu Ile Asp Ala Pro Lys Asn Leu Arg Val Gly Ser Arg Thr Ala Thr
            595                 600                 605

Ser Leu Asp Leu Glu Trp Asp Asn Ser Glu Ala Glu Val Gln Glu Tyr
    610                 615                 620

Lys Val Val Tyr Ser Thr Leu Ala Gly Glu Gln Tyr His Glu Val Leu
625                 630                 635                 640

Val Pro Arg Gly Ile Gly Pro Thr Thr Arg Ala Thr Leu Thr Asp Leu
            645                 650                 655

Val Pro Gly Thr Glu Tyr Gly Val Gly Ile Ser Ala Val Met Asn Ser
            660                 665                 670

Gln Gln Ser Val Pro Ala Thr Met Asn Ala Arg Thr Glu Leu Asp Ser
            675                 680                 685

Pro Arg Asp Leu Met Val Thr Ala Ser Ser Glu Thr Ser Ile Ser Leu
    690                 695                 700
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Ile Trp Thr Lys Ala Ser Gly Pro Ile Asp His Tyr Arg Ile Thr Phe
705             710         715             720

Thr Pro Ser Ser Gly Ile Ala Ser Glu Val Thr Val Pro Lys Asp Arg
            725         730             735

Thr Ser Tyr Thr Leu Thr Asp Leu Glu Pro Gly Ala Glu Tyr Ile Ile
        740             745             750

Ser Val Thr Ala Glu Arg Gly Arg Gln Gln Ser Leu Glu Ser Thr Val
    755             760             765

Asp Ala Phe Thr Gly Phe Arg Pro Ile Ser His Leu His Phe Ser His
    770             775             780

Val Thr Ser Ser Ser Val Asn Ile Thr Trp Ser Asp Pro Ser Pro Pro
785             790             795             800

Ala Asp Arg Leu Ile Leu Asn Tyr Ser Pro Arg Asp Glu Glu Glu Glu
            805             810             815

Met Met Glu Val Ser Leu Asp Ala Thr Lys Arg His Ala Val Leu Met
            820             825             830

Gly Leu Gln Pro Ala Thr Glu Tyr Ile Val Asn Leu Val Ala Val His
    835             840             845

Gly Thr Val Thr Ser Glu Pro Ile Val Gly Ser Ile Thr Thr Gly Ile
    850             855             860

Asp Pro Pro Lys Asp Ile Thr Ile Ser Asn Val Thr Lys Asp Ser Val
865             870             875             880

Met Val Ser Trp Ser Pro Pro Val Ala Ser Phe Asp Tyr Tyr Arg Val
            885             890             895

Ser Tyr Arg Pro Thr Gln Val Gly Arg Leu Asp Ser Ser Val Val Pro
        900             905             910

Asn Thr Val Thr Glu Phe Thr Ile Thr Arg Leu Asn Pro Ala Thr Glu
        915             920             925

Tyr Glu Ile Ser Leu Asn Ser Val Arg Gly Arg Glu Glu Ser Glu Arg
    930             935             940

Ile Cys Thr Leu Val His Thr Ala Met Asp Asn Pro Val Asp Leu Ile
945             950             955             960

Ala Thr Asn Ile Thr Pro Thr Glu Ala Leu Leu Gln Trp Lys Ala Pro
            965             970             975

Val Gly Glu Val Glu Asn Tyr Val Ile Val Leu Thr His Phe Ala Val
            980             985             990

Ala Gly Glu Thr Ile Leu Val Asp  Gly Val Ser Glu Glu  Phe Arg Leu
    995             1000             1005
```

12

```
Val Asp   Leu Leu Pro Ser Thr   His Tyr Thr Ala Thr   Met Tyr Ala
    1010              1015               1020

Thr Asn   Gly Pro Leu Thr Ser   Gly Thr Ile Ser Thr   Asn Phe Ser
    1025              1030               1035

Thr Leu   Leu Asp Pro Pro Ala   Asn Leu Thr Ala Ser   Glu Val Thr
    1040              1045               1050

Arg Gln   Ser Ala Leu Ile Ser   Trp Gln Pro Pro Arg   Ala Glu Ile
    1055              1060               1065

Glu Asn   Tyr Val Leu Thr Tyr   Lys Ser Thr Asp Gly   Ser Arg Lys
    1070              1075               1080

Glu Leu   Ile Val Asp Ala Glu   Asp Thr Trp Ile Arg   Leu Glu Gly
    1085              1090               1095

Leu Leu   Glu Asn Thr Asp Tyr   Thr Val Leu Leu Gln   Ala Ala Gln
    1100              1105               1110

Asp Thr   Thr Trp Ser Ser Ile   Thr Ser Thr Ala Phe   Thr Thr Gly
    1115              1120               1125

Gly Arg   Val Phe Pro His Pro   Gln Asp Cys Ala Gln   His Leu Met
    1130              1135               1140

Asn Gly   Asp Thr Leu Ser Gly   Val Tyr Pro Ile Phe   Leu Asn Gly
    1145              1150               1155

Glu Leu   Ser Gln Lys Leu Gln   Val Tyr Cys Asp Met   Thr Thr Asp
    1160              1165               1170

Gly Gly   Gly Trp Ile Val Phe   Gln Arg Arg Gln Asn   Gly Gln Thr
    1175              1180               1185

Asp Phe   Phe Arg Lys Trp Ala   Asp Tyr Arg Val Gly   Phe Gly Asn
    1190              1195               1200

Val Glu   Asp Glu Phe Trp Leu   Gly Leu Asp Asn Ile   His Arg Ile
    1205              1210               1215

Thr Ser   Gln Gly Arg Tyr Glu   Leu Arg Val Asp Met   Arg Asp Gly
    1220              1225               1230

Gln Glu   Ala Ala Phe Ala Ser   Tyr Asp Arg Phe Ser   Val Glu Asp
    1235              1240               1245

Ser Arg   Asn Leu Tyr Lys Leu   Arg Ile Gly Ser Tyr   Asn Gly Thr
    1250              1255               1260

Ala Gly   Asp Ser Leu Ser Tyr   His Gln Gly Arg Pro   Phe Ser Thr
    1265              1270               1275

Glu Asp   Arg Asp Asn Asp Val   Ala Val Thr Asn Cys   Ala Met Ser
    1280              1285               1290
```

13

Tyr Lys Gly Ala Trp Trp Tyr Lys Asn Cys His Arg Thr Asn Leu
    1295   1300   1305

Asn Gly Lys Tyr Gly Glu Ser Arg His Ser Gln Gly Ile Asn Trp
    1310   1315   1320

Tyr His Trp Lys Gly His Glu Phe Ser Ile Pro Phe Val Glu Met
    1325   1330   1335

Lys Met Arg Pro Tyr Asn His Arg Leu Met Ala Gly Arg Lys Arg
    1340   1345   1350

Gln Ser Leu Gln Phe
    1355